

2/19

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/047,257

DATE: 02/28/2002

TIME: 12:47:47

Input Set : A:\CHO\_D06.APP.txt

Output Set: N:\CRF3\02282002\J047257.raw

3 <110> APPLICANT: Cho, Myung-Sam  
 4 Chan, Sham-Yuen  
 5 Kelsey, William  
 6 Yee, Helena  
 8 <120> TITLE OF INVENTION: Expression System for Factor VIII  
 10 <130> FILE REFERENCE: MSB-7255.2  
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/047,257  
 C--> 13 <141> CURRENT FILING DATE: 2002-01-15  
 15 <160> NUMBER OF SEQ ID NOS: 2  
 17 <170> SOFTWARE: PatentIn Ver. 2.0  
 19 <210> SEQ ID NO: 1  
 20 <211> LENGTH: 1438  
 21 <212> TYPE: PRT  
 22 <213> ORGANISM: Artificial Sequence  
 24 <220> FEATURE:  
 26 <223> OTHER INFORMATION: Description of Artificial Sequence: Derived from  
 27 human factor VIII sequence  
 29 <400> SEQUENCE: 1  
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 32 1 5 10 15  
 34 Met Gln Ser Asp Leu Gly Glu Leu Pro Val Asp Ala Arg Phe Pro Pro  
 35 20 25 30  
 37 Arg Val Pro Lys Ser Phe Pro Phe Asn Thr Ser Val Val Tyr Lys Lys  
 38 35 40 45  
 40 Thr Leu Phe Val Glu Phe Thr Val His Leu Phe Asn Ile Ala Lys Pro  
 41 50 55 60  
 43 Arg Pro Pro Trp Met Gly Leu Leu Gly Pro Thr Ile Gln Ala Glu Val  
 44 65 70 75 80  
 46 Tyr Asp Thr Val Val Ile Thr Leu Lys Asn Met Ala Ser His Pro Val  
 47 85 90 95  
 49 Ser Leu His Ala Val Gly Val Ser Tyr Trp Lys Ala Ser Glu Gly Ala  
 50 100 105 110  
 52 Glu Tyr Asp Asp Gln Thr Ser Gln Arg Glu Lys Glu Asp Asp Lys Val  
 53 115 120 125  
 55 Phe Pro Gly Gly Ser His Thr Tyr Val Trp Gln Val Leu Lys Glu Asn  
 56 130 135 140  
 58 Gly Pro Met Ala Ser Asp Pro Leu Cys Leu Thr Tyr Ser Tyr Leu Ser  
 59 145 150 155 160  
 61 His Val Asp Leu Val Lys Asp Leu Asn Ser Gly Leu Ile Gly Ala Leu  
 62 165 170 175  
 64 Leu Val Cys Arg Glu Gly Ser Leu Ala Lys Glu Lys Thr Gln Thr Leu  
 65 180 185 190  
 67 His Lys Phe Ile Leu Leu Phe Ala Val Phe Asp Glu Gly Lys Ser Trp

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68          195          200          205
70 His Ser Glu Thr Lys Asn Ser Leu Met Gln Asp Arg Asp Ala Ala Ser
71          210          215          220
73 Ala Arg Ala Trp Pro Lys Met His Thr Val Asn Gly Tyr Val Asn Arg
74 225          230          235          240
76 Ser Leu Pro Gly Leu Ile Gly Cys His Arg Lys Ser Val Tyr Trp His
77          245          250          255
79 Val Ile Gly Met Gly Thr Thr Pro Glu Val His Ser Ile Phe Leu Glu
80          260          265          270
82 Gly His Thr Phe Leu Val Arg Asn His Arg Gln Ala Ser Leu Glu Ile
83          275          280          285
85 Ser Pro Ile Thr Phe Leu Thr Ala Gln Thr Leu Leu Met Asp Leu Gly
86          290          295          300
88 Gln Phe Leu Leu Phe Cys His Ile Ser Ser His Gln His Asp Gly Met
89 305          310          315          320
91 Glu Ala Tyr Val Lys Val Asp Ser Cys Pro Glu Glu Pro Gln Leu Arg
92          325          330          335
94 Met Lys Asn Asn Glu Glu Ala Glu Asp Tyr Asp Asp Asp Leu Thr Asp
95          340          345          350
97 Ser Glu Met Asp Val Val Arg Phe Asp Asp Asp Asn Ser Pro Ser Phe
98          355          360          365
100 Ile Gln Ile Arg Ser Val Ala Lys Lys His Pro Lys Thr Trp Val His
101          370          375          380
103 Tyr Ile Ala Ala Glu Glu Glu Asp Trp Asp Tyr Ala Pro Leu Val Leu
104 385          390          395          400
106 Ala Pro Asp Asp Arg Ser Tyr Lys Ser Gln Tyr Leu Asn Asn Gly Pro
107          405          410          415
109 Gln Arg Ile Gly Arg Lys Tyr Lys Lys Val Arg Phe Met Ala Tyr Thr
110          420          425          430
112 Asp Glu Thr Phe Lys Thr Arg Glu Ala Ile Gln His Glu Ser Gly Ile
113          435          440          445
115 Leu Gly Pro Leu Leu Tyr Gly Glu Val Gly Asp Thr Leu Leu Ile Ile
116          450          455          460
118 Phe Lys Asn Gln Ala Ser Arg Pro Tyr Asn Ile Tyr Pro His Gly Ile
119 465          470          475          480
121 Thr Asp Val Arg Pro Leu Tyr Ser Arg Arg Leu Pro Lys Gly Val Lys
122          485          490          495
124 His Leu Lys Asp Phe Pro Ile Leu Pro Gly Glu Ile Phe Lys Tyr Lys
125          500          505          510
127 Trp Thr Val Thr Val Glu Asp Gly Pro Thr Lys Ser Asp Pro Arg Cys
128          515          520          525
130 Leu Thr Arg Tyr Tyr Ser Ser Phe Val Asn Met Glu Arg Asp Leu Ala
131          530          535          540
133 Ser Gly Leu Ile Gly Pro Leu Leu Ile Cys Tyr Lys Glu Ser Val Asp
134 545          550          555          560
136 Gln Arg Gly Asn Gln Ile Met Ser Asp Lys Arg Asn Val Ile Leu Phe
137          565          570          575
139 Ser Val Phe Asp Glu Asn Arg Ser Trp Tyr Leu Thr Glu Asn Ile Gln
140          580          585          590

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142 Arg Phe Leu Pro Asn Pro Ala Gly Val Gln Leu Glu Asp Pro Glu Phe
143          595          600          605
145 Gln Ala Ser Asn Ile Met His Ser Ile Asn Gly Tyr Val Phe Asp Ser
146      610          615          620
148 Leu Gln Leu Ser Val Cys Leu His Glu Val Ala Tyr Trp Tyr Ile Leu
149 625          630          635          640
151 Ser Ile Gly Ala Gln Thr Asp Phe Leu Ser Val Phe Phe Ser Gly Tyr
152          645          650          655
154 Thr Phe Lys His Lys Met Val Tyr Glu Asp Thr Leu Thr Leu Phe Pro
155          660          665          670
157 Phe Ser Gly Glu Thr Val Phe Met Ser Met Glu Asn Pro Gly Leu Trp
158      675          680          685
160 Ile Leu Gly Cys His Asn Ser Asp Phe Arg Asn Arg Gly Met Thr Ala
161      690          695          700
163 Leu Leu Lys Val Ser Ser Cys Asp Lys Asn Thr Gly Asp Tyr Tyr Glu
164 705          710          715          720
166 Asp Ser Tyr Glu Asp Ile Ser Ala Tyr Leu Leu Ser Lys Asn Asn Ala
167          725          730          735
169 Ile Glu Pro Arg Ser Phe Ser Gln Asn Pro Pro Val Leu Lys Arg His
170          740          745          750
172 Gln Arg Glu Ile Thr Arg Thr Thr Leu Gln Ser Asp Gln Glu Glu Ile
173          755          760          765
175 Asp Tyr Asp Asp Thr Ile Ser Val Glu Met Lys Lys Glu Asp Phe Asp
176      770          775          780
178 Ile Tyr Asp Glu Asp Glu Asn Gln Ser Pro Arg Ser Phe Gln Lys Lys
179 785          790          795          800
181 Thr Arg His Tyr Phe Ile Ala Ala Val Glu Arg Leu Trp Asp Tyr Gly
182          805          810          815
184 Met Ser Ser Ser Pro His Val Leu Arg Asn Arg Ala Gln Ser Gly Ser
185          820          825          830
187 Val Pro Gln Phe Lys Lys Val Val Phe Gln Glu Phe Thr Asp Gly Ser
188      835          840          845
190 Phe Thr Gln Pro Leu Tyr Arg Gly Glu Leu Asn Glu His Leu Gly Leu
191      850          855          860
193 Leu Gly Pro Tyr Ile Arg Ala Glu Val Glu Asp Asn Ile Met Val Thr
194 865          870          875          880
196 Phe Arg Asn Gln Ala Ser Arg Pro Tyr Ser Phe Tyr Ser Ser Leu Ile
197          885          890          895
199 Ser Tyr Glu Glu Asp Gln Arg Gln Gly Ala Glu Pro Arg Lys Asn Phe
200          900          905          910
202 Val Lys Pro Asn Glu Thr Lys Thr Tyr Phe Trp Lys Val Gln His His
203          915          920          925
205 Met Ala Pro Thr Lys Asp Glu Phe Asp Cys Lys Ala Trp Ala Tyr Phe
206      930          935          940
208 Ser Asp Val Asp Leu Glu Lys Asp Val His Ser Gly Leu Ile Gly Pro
209 945          950          955          960
211 Leu Leu Val Cys His Thr Asn Thr Leu Asn Pro Ala His Gly Arg Gln
212          965          970          975
214 Val Thr Val Gln Glu Phe Ala Leu Phe Phe Thr Ile Phe Asp Glu Thr

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215          980          985          990
217 Lys Ser Trp Tyr Phe Thr Glu Asn Met Glu Arg Asn Cys Arg Ala Pro
218          995          1000          1005
220 Cys Asn Ile Gln Met Glu Asp Pro Thr Phe Lys Glu Asn Tyr Arg Phe
221      1010          1015          1020
223 His Ala Ile Asn Gly Tyr Ile Met Asp Thr Leu Pro Gly Leu Val Met
224 1025          1030          1035          1040
226 Ala Gln Asp Gln Arg Ile Arg Trp Tyr Leu Leu Ser Met Gly Ser Asn
227          1045          1050          1055
229 Glu Asn Ile His Ser Ile His Phe Ser Gly His Val Phe Thr Val Arg
230          1060          1065          1070
232 Lys Lys Glu Glu Tyr Lys Met Ala Leu Tyr Asn Leu Tyr Pro Gly Val
233      1075          1080          1085
235 Phe Glu Thr Val Glu Met Leu Pro Ser Lys Ala Gly Ile Trp Arg Val
236      1090          1095          1100
238 Glu Cys Leu Ile Gly Glu His Leu His Ala Gly Met Ser Thr Leu Phe
239 1105          1110          1115          1120
241 Leu Val Tyr Ser Asn Lys Cys Gln Thr Pro Leu Gly Met Ala Ser Gly
242          1125          1130          1135
244 His Ile Arg Asp Phe Gln Ile Thr Ala Ser Gly Gln Tyr Gly Gln Trp
245          1140          1145          1150
247 Ala Pro Lys Leu Ala Arg Leu His Tyr Ser Gly Ser Ile Asn Ala Trp
248          1155          1160          1165
250 Ser Thr Lys Glu Pro Phe Ser Trp Ile Lys Val Asp Leu Leu Ala Pro
251      1170          1175          1180
253 Met Ile Ile His Gly Ile Lys Thr Gln Gly Ala Arg Gln Lys Phe Ser
254 1185          1190          1195          1200
256 Ser Leu Tyr Ile Ser Gln Phe Ile Ile Met Tyr Ser Leu Asp Gly Lys
257          1205          1210          1215
259 Lys Trp Gln Thr Tyr Arg Gly Asn Ser Thr Gly Thr Leu Met Val Phe
260          1220          1225          1230
262 Phe Gly Asn Val Asp Ser Ser Gly Ile Lys His Asn Ile Phe Asn Pro
263          1235          1240          1245
265 Pro Ile Ile Ala Arg Tyr Ile Arg Leu His Pro Thr His Tyr Ser Ile
266      1250          1255          1260
268 Arg Ser Thr Leu Arg Met Glu Leu Met Gly Cys Asp Leu Asn Ser Cys
269 1265          1270          1275          1280
271 Ser Met Pro Leu Gly Met Glu Ser Lys Ala Ile Ser Asp Ala Gln Ile
272          1285          1290          1295
274 Thr Ala Ser Ser Tyr Phe Thr Asn Met Phe Ala Thr Trp Ser Pro Ser
275          1300          1305          1310
277 Lys Ala Arg Leu His Leu Gln Gly Arg Ser Asn Ala Trp Arg Pro Gln
278          1315          1320          1325
280 Val Asn Asn Pro Lys Glu Trp Leu Gln Val Asp Phe Gln Lys Thr Met
281      1330          1335          1340
283 Lys Val Thr Gly Val Thr Gln Gly Val Lys Ser Leu Leu Thr Ser
284 1345          1350          1355          1360
286 Met Tyr Val Lys Glu Phe Leu Ile Ser Ser Ser Gln Asp Gly His Gln
287          1365          1370          1375

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289 Trp Thr Leu Phe Phe Gln Asn Gly Lys Val Lys Val Phe Gln Gly Asn
290          1380          1385          1390
292 Gln Asp Ser Phe Thr Pro Val Val Asn Ser Leu Asp Pro Pro Leu Leu
293          1395          1400          1405
295 Thr Arg Tyr Leu Arg Ile His Pro Gln Ser Trp Val His Gln Ile Ala
296          1410          1415          1420
298 Leu Arg Met Glu Val Leu Gly Cys Glu Ala Gln Asp Leu Tyr
299 1425          1430          1435
302 <210> SEQ ID NO: 2
303 <211> LENGTH: 402
304 <212> TYPE: DNA
305 <213> ORGANISM: Artificial Sequence
307 <220> FEATURE:
308 <223> OTHER INFORMATION: Description of Artificial Sequence:Derived from
309      Epstein-Barr virus sequence
311 <400> SEQUENCE: 2
312 ggcaatggag cgtgacgaag ggccccaggg ctgaccccg caaacgtgac ccggggctcc 60
313 ggggtgaccc aggcaagcgt ggccaagggg cccgtgggtg acacaggcaa ccctgacaaa 120
314 ggccccccag gaaagacccc cggggggcat cgggggggtg ttggcgggtc atgggggggg 180
315 cgggtcatgc cgcgcattcc tggaaaaagt ggagggggcg tggccttccc ccgcggcccc 240
316 cctagccccc ccgcagagag cggcgcaacg gcgggcgagc ggcggggggg cggggtccgc 300
317 gggctccggg ggctgcgggc ggtggatggc ggctggcgtt ccggggatcg ggggggggtc 360
318 gggggggcgt gcgcgggcgc agccatgcgt gaccgtgatg ag 402

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/047,257

DATE: 02/28/2002

TIME: 12:47:48

Input Set : A:\CHO\_D06.APP.txt

Output Set: N:\CRF3\02282002\J047257.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date